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|-------------------------|------------------------------------|----------------------------|--|
| Notice to Comply | Application No. 10526028 | Applicant(s) LIU ET AL. | |
| | Examiner Andrew D. Kosar | Art Unit 1654 | |

NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS CONTAINING NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE DISCLOSURES

Applicant must file the items indicated below within the time period set the Office action to which the Notice is attached to avoid abandonment under 35 U.S.C. § 133 (extensions of time may be obtained under the provisions of 37 CFR 1.136(a)).

The nucleotide and/or amino acid sequence disclosure contained in this application does not comply with the requirements for such a disclosure as set forth in 37 C.F.R. 1.821 - 1.825 for the following reason(s):

- ☒ 1. This application clearly fails to comply with the requirements of 37 C.F.R. 1.821-1.825. Applicant's attention is directed to the final rulemaking notice published at 55 FR 18230 (May 1, 1990), and 1114 OG 29 (May 15, 1990). If the effective filing date is on or after July 1, 1998, see the final rulemaking notice published at 63 FR 29620 (June 1, 1998) and 1211 OG 82 (June 23, 1998).
- ☐ 2. This application does not contain, as a separate part of the disclosure on paper copy, a "Sequence Listing" as required by 37 C.F.R. 1.821(c).
- ☐ 3. A copy of the "Sequence Listing" in computer readable form has not been submitted as required by 37 C.F.R. 1.821(e).
- ☒ 4. A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 C.F.R. 1.822 and/or 1.823, as indicated on the attached copy of the marked -up "Raw Sequence Listing."
- ☐ 5. The computer readable form that has been filed with this application has been found to be damaged and/or unreadable as indicated on the attached CRF Diskette Problem Report. A Substitute computer readable form must be submitted as required by 37 C.F.R. 1.825(d).
- ☐ 6. The paper copy of the "Sequence Listing" is not the same as the computer readable form of the "Sequence Listing" as required by 37 C.F.R. 1.821(e).
- ☐ 7. Other:

Applicant Must Provide:

- ☒ An initial or substitute computer readable form (CRF) copy of the "Sequence Listing".
- ☒ An initial or substitute paper copy of the "Sequence Listing", as well as an amendment directing its entry into the specification.
- ☒ A statement that the content of the paper and computer readable copies are the same and, where applicable, include no new matter, as required by 37 C.F.R. 1.821(e) or 1.821(f) or 1.821(g) or 1.825(b) or 1.825(d).

For questions regarding compliance to these requirements, please contact:

For Rules Interpretation, call (703) 308-4216 or (703) 308-2923

For CRF Submission Help, call (703) 308-4212 or 308-2923

PatentIn Software Program Support

Technical Assistance.....703-287-0200

To Purchase PatentIn Software.....703-306-2600

PLEASE RETURN A COPY OF THIS NOTICE WITH YOUR REPLY

STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/526,028
Source: IFWO
Date Processed by STIC: 4/5/07

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.4.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chknote.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

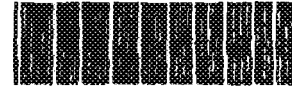
Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/efb/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):
U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/10/06

Raw Sequence Listing Error Summary

| ERROR DETECTED | SUGGESTED CORRECTION | SERIAL NUMBER: 10/526,028 |
|--|--|---------------------------|
| ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE | | |
| 1 ____ Wrapped Nucleics Wrapped Aminos | The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to 3; this will prevent "wrapping." | |
| 2 ____ Invalid Line Length | The rules require that a line not exceed 72 characters in length. This includes white spaces. | |
| 3 ____ Misaligned Amino Numbering | The numbering under each 3 rd amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead. | |
| 4 ____ Non-ASCII | The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text. | |
| 5 ____ Variable Length | Sequence(s) ____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing. | |
| 6 ____ PatentIn 2.0 "bug" | A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <228>-<233> sections for Artificial or Unknown sequences. | |
| 7 ____ Skipped Sequences (OLD RULES) | Sequence(s) ____ missing. If intentional, please insert the following lines for each skipped sequence: (i) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) (ii) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading) (iii) SEQUENCE DESCRIPTION: SEQ ID NO:X: (insert SEQ ID NO where "X" is shown). This sequence is intentionally skipped. Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences. | |
| 8 ____ Skipped Sequences (NEW RULES) | Sequence(s) ____ missing. If intentional, please insert the following lines for each skipped sequence: <210> sequence id number <400> sequence id number 000 | |
| 9 ____ Use of n's or Xaa's (NEW RULES) | Use of n's and/or Xaa's have been detected in the Sequence Listing. Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of a n or Xaa, and which residue n or Xaa represents. | |
| 10 ____ Invalid <213> Response | Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence. (see item 11 below) | |
| 11 ____ Use of <220> | Sequence(s) ____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section or use "chemically synthesized" as explanation. (See "Federal Register," 6601/1998, Vol. 63, No. 104, pp. 29631-32, also Sec. 1.823 of Sequence Rules) | |
| 12 ____ PatentIn 2.0 "bug" | Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk. | |
| 13 ____ Misuse of n/Xaa | "n" can only represent a single nucleotide; "Xaa" can only represent a single amino acid | |



IPWO

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/526,028

DATE: 04/05/2007
TIME: 07:41:22

Input Set : A:\186326 us.ST25.txt
Output Set: M:\CRF4\04052007\J526028.raw

3 <110> APPLICANT: Liu, Zhihui
4 Lu, Yi
5 Chen, Zhongwei
6 Shi, Deyuan
7 Cui, Dafu
9 <120> TITLE OF INVENTION: THE SYNERGISTIC EFFECT OF OGP AND G-CSF ON HAEMATOGENESIS
11 <130> FILE REFERENCE: 186326/US
13 <140> CURRENT APPLICATION NUMBER: 10/526,028
14 <141> CURRENT FILING DATE: 2005-02-28
16 <160> NUMBER OF SEQ ID NOS: 1
18 <170> SOFTWARE: PatentIn version 3.3
20 <210> SEQ ID NO: 1
21 <211> LENGTH: 14
22 <212> TYPE: PRT
23 <213> ORGANISM: Artificial
25 <220> FEATURE:
26 <223> OTHER INFORMATION: oligonucleotide *this is not an oligonucleotide sequence.*
28 <400> SEQUENCE: 1
30 Ala Leu Lys Arg Gln Gly Arg Thr Leu Tyr Gly Phe Gly Gly
31 1 5 10

Does Not Comply
Corrected Dikette Needed

*Please indicate
source of genetic
material. See
item 11 on Euro
summary sheet.*

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/526,028

DATE: 04/05/2007

TIME: 07:41:23

Input Set : A:\186326 us.ST25.txt

Output Set: H:\CRF4\04052007\J526028.raw